



SEQUENCE LISTING

<110> Potter, Robert
Rosenthal, Kim

<120> High Fidelity Reverse Transcriptases and Uses Thereof

<130> 0942.5030001/RWE

<140> 09/808,124

<141> 2001-03-15

<150> 60/189,454

<151> 2000-03-15

<160> 6

<170> PatentIn version 3.0

<210> 1

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide template

<400> 1

gagttacagt gtttttggtc cagtctgtag cagtgtgtga atggaag

47

<210> 2

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide primer

<400> 2

cttccattca cacactgc

18

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide primer

<400> 3

gaagatcgca ctccagccag c

21

<210> 4

<211> 298

<212> DNA

<213> Artificial Sequence

<220>

<223> lacZ α peptide in M13mp19 from SuperScript II RT and
SuperScript II H203R T306K F309N

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agcgcaacgc aattaatgtg agttagctca ctcataggc accccaggct ttacacttta 60

tgcttccggc tcgtatgttg tgtggaattg tgagcggata acaatttcac acaggaaaca 120

gctatgacca tgattacgcc aagcttgcac gcctgcaggt cgactctaga ggatccccgg 180

gtaccgagct cgaattcact ggccgtcgtt ttacaacgtc gtgactggga aaaccctggc	240
gttaccacaac ttaatcgctt tgcagcacat ccccttttcg ccagctggcg taatagcg	298

<210> 5

<211> 1575

<212> DNA

<213> Moloney-Murine Leukemia Virus

<220>

<221> CDS

<222> (1) .. (1575)

<400> 5

atg acc cta aat ata gaa gat gag cat cgg cta cat gag acc tca aaa	48
Met Thr Leu Asn Ile Glu Asp Glu His Arg Leu His Glu Thr Ser Lys	
1 5 10 15	
gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag	96
Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln	
20 25 30	
gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct	144
Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro	
35 40 45	
ctg atc ata cct ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa	192
Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln	
50 55 60	
tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag	240
Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln	
65 70 75 80	
aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac	288
Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn	
85 90 95	
acg ccc ctg cta ccc gtt aag aaa cca ggg act aat gat tat agg cct	336
Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro	
100 105 110	
gtc cag gat ctg aga gaa gtc aac aag cgg gtg gaa gac atc cac ccc	384
Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro	
115 120 125	
acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc aag cgg gtg gaa	432

Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Lys	Arg	Val	Glu		
130						135					140						
gac	atc	cac	ccc	acc	gtg	ccc	aac	cct	tac	aac	ctc	ttg	agc	ggg	ctc	480	
Asp	Ile	His	Pro	Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu		
145					150					155					160		
cca	ccg	tcc	cac	cag	tgg	tac	act	gtg	ctt	gat	tta	aag	gat	gcc	ttt	528	
Pro	Pro	Ser	His	Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Phe		
				165					170					175			
ttc	tgc	ctg	aga	ctc	cac	ccc	acc	agt	cag	cct	ctc	ttc	gcc	ttt	gag	576	
Phe	Cys	Leu	Arg	Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu		
			180					185					190				
tgg	aga	gat	cca	gag	atg	gga	atc	tca	gga	caa	ttg	acc	tgg	acc	aga	624	
Trp	Arg	Asp	Pro	Glu	Met	Gly	Ile	Ser	Gly	Gln	Leu	Thr	Trp	Thr	Arg		
		195					200					205					
ctc	cca	cag	ggg	ttc	aaa	aac	agt	ccc	acc	ctg	ttt	gat	gag	gca	ctg	672	
Leu	Pro	Gln	Gly	Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu		
	210					215					220						
cac	aga	gac	cta	gca	gac	ttc	cgg	atc	cag	cac	cca	gac	ttg	atc	ctg	720	
His	Arg	Asp	Leu	Ala	Asp	Phe	Arg	Ile	Gln	His	Pro	Asp	Leu	Ile	Leu		
225					230					235					240		
cta	cag	tac	gtg	gat	gac	tta	ctg	ctg	gcc	gcc	act	tct	gag	cta	gac	768	
Leu	Gln	Tyr	Val	Asp	Asp	Leu	Leu	Leu	Ala	Ala	Thr	Ser	Glu	Leu	Asp		
				245					250					255			
tgc	caa	caa	ggg	act	cgg	gcc	ctg	tta	caa	acc	cta	ggg	aac	ctc	ggg	816	
Cys	Gln	Gln	Gly	Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asn	Leu	Gly		
			260					265					270				
tat	cgg	gcc	tcg	gcc	aag	aaa	gcc	caa	att	tgc	cag	aaa	cag	gtc	aag	864	
Tyr	Arg	Ala	Ser	Ala	Lys	Lys	Ala	Gln	Ile	Cys	Gln	Lys	Gln	Val	Lys		
		275					280					285					
tat	ctg	ggg	tat	ctt	cta	aaa	gag	ggg	cag	aga	tgg	ctg	act	gag	gcc	912	
Tyr	Leu	Gly	Tyr	Leu	Leu	Lys	Glu	Gly	Gln	Arg	Trp	Leu	Thr	Glu	Ala		
	290					295					300						
aga	aaa	gag	act	gtg	atg	ggg	cag	cct	act	ccg	aag	acc	cct	cga	caa	960	
Arg	Lys	Glu	Thr	Val	Met	Gly	Gln	Pro	Thr	Pro	Lys	Thr	Pro	Arg	Gln		
305					310					315					320		
cta	agg	gag	ttc	cta	ggg	acg	gca	ggc	ttc	tgt	cgc	ctc	tgg	atc	cct	1008	
Leu	Arg	Glu	Phe	Leu	Gly	Thr	Ala	Gly	Phe	Cys	Arg	Leu	Trp	Ile	Pro		
				325					330					335			
ggg	ttt	gca	gaa	atg	gca	gcc	ccc	ttg	tac	cct	ctc	acc	aaa	acg	ggg	1056	
Gly	Phe	Ala	Glu	Met	Ala	Ala	Pro	Leu	Tyr	Pro	Leu	Thr	Lys	Thr	Gly		
			340					345					350				
act	ctg	ttt	aat	tgg	ggc	cca	gac	caa	caa	aag	gcc	tat	caa	gaa	atc	1104	
Thr	Leu	Phe	Asn	Trp	Gly	Pro	Asp	Gln	Gln	Lys	Ala	Tyr	Gln	Glu	Ile		

355	360	365	
aag caa gct ctt cta act gcc cca gcc ctg ggg ttg cca gat ttg act			1152
Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr			
370	375	380	
aag ccc ttt gaa ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt			1200
Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly			
385	390	395	400
gtc cta acg caa aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg			1248
Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu			
	405	410	415
tcc aaa aag cta gac cca gta gca gct ggg tgg ccc cct tgc cta cgg			1296
Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg			
	420	425	430
atg gta gca gcc att gcc gta ctg aca aag gat gca ggc aag cta acc			1344
Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr			
	435	440	445
atg gga cag cca cta gtc att ctg gcc ccc cat gca gta gag gca cta			1392
Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu			
	450	455	460
gtc aaa caa ccc ccc gac cgc tgg ctt tcc aac gcc cgg atg act cac			1440
Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His			
	465	470	475
tat cag gcc ttg ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg			1488
Tyr Gln Ala Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val			
	485	490	495
gta gcc ctg aac ccg gct acg ctg ctc cca ctg cct gag gaa ggg ctg			1536
Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu			
	500	505	510
caa cac aac tgc ctt gat aat tcc cgc tta att aat taa			1575
Gln His Asn Cys Leu Asp Asn Ser Arg Leu Ile Asn			
	515	520	

<210> 6

<211> 524

<212> PRT

<213> Moloney-Murine Leukemia Virus

<400> 6

Met	Thr	Leu	Asn	Ile	Glu	Asp	Glu	His	Arg	Leu	His	Glu	Thr	Ser	Lys
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Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
 20 25 30

Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
 35 40 45

Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
 50 55 60

Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
 65 70 75 80

Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
 85 90 95

Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
 100 105 110

Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
 115 120 125

Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Lys Arg Val Glu
 130 135 140

Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu
 145 150 155 160

Pro Pro Ser His Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe
 165 170 175

Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu
 180 185 190

Trp Arg Asp Pro Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg
 195 200 205

Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu
 210 215 220

His Arg Asp Leu Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu
 225 230 235 240

Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp
 245 250 255

Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly
 260 265 270

Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys
 275 280 285

Tyr Leu Gly Tyr Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala
 290 295 300

Arg Lys Glu Thr Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln
 305 310 315 320

Leu Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro
 325 330 335

Gly Phe Ala Glu Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly
 340 345 350

Thr Leu Phe Asn Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile
 355 360 365

Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr
 370 375 380

Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly
 385 390 395 400

Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu
 405 410 415

Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg
 420 425 430

Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr
 435 440 445

Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu
 450 455 460

Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His

465

470

475

480

Tyr Gln Ala Leu Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val
485 490 495

Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu
500 505 510

Gln His Asn Cys Leu Asp Asn Ser Arg Leu Ile Asn
515 520